

TABLE 30					
Genes Corresponding To Differentially Expressed Genes in Figure 22 - Osteoarthritis					
Spot	p-value	Description	Accession	Unigene	Protein Accession No.
8	0.000153	calreticulin (CALR), mRNA /cds=(69,1322) /gb=NM_004343 /gi=5921996 /ug=Hs.353170 /len=1899	NM_004343	Hs.353170	NP_004334
21	0.000298	telomeric repeat binding factor (NIMA-interacting) 1 (TERF1), transcript variant 1, mRNA /cds=(16,1335) /gb=NM_017489 /gi=9257245 /ug=Hs.194562 /len=2686	NM_017489	Hs.194562	NP_059523
91	0.001116	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
146	0.001393	similar to hypothetical protein (L1H 3 region) - human (LOC201853), mRNA /cds=(500,820) /gb=NM_145302 /gi=21699085 /ug=Hs.343206 /len=851	NM_145302	Hs.343206	NP_660345.1
176	0.000508	nuclear autoantigenic sperm protein (histone-binding) (NASP), transcript variant 1, mRNA /cds=(170,2542) /gb=NM_172164 /gi=27262633 /ug=Hs.380400 /len=3396	NM_172164	Hs.380400	NP_751896
192	0.000809	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948	BAA25496.2
195	0.000346	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa) (XRCC5), mRNA /cds=(34,2232) /gb=NM_021141 /gi=12408650 /ug=Hs.84981 /len=3310	NM_021141	Hs.84981	NP_066964
301	0.000333	chaperonin containing TCP1, subunit 4 (delta) (CCT4), mRNA /cds=(1,1620) /gb=NM_006430 /gi=5453604 /ug=Hs.79150 /len=1883	NM_006430	Hs.79150	NP_006421
328	0.001746	EST(yj40f11.r1 clone 151245 5')	H02533		NP_705833
331	0.000492	dihydropyrimidinase-like 2 (DPYSL2), mRNA /cds=(275,1993) /gb=NM_001386 /gi=19923654 /ug=Hs.173381 /len=4459	NM_001386	Hs.173381	NP_001377
333	8.88E-06	chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA /cds=(29,1675) /gb=NM_006585 /gi=6005726 /ug=Hs.15071 /len=1821	NM_006585	Hs.15071	NP_006576
361	0.001546	THO complex 1 (THOC1), mRNA /cds=(15,1988) /gb=NM_005131 /gi=4826881 /ug=Hs.1540 /len=2092	NM_005131	Hs.1540	NP_005122

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Spot	p-value	Description	Accession	Unigene	Protein Accession No.
405	0.001541	ATPase, Ca transporting, plasma membrane 1 (ATP2B1), mRNA /cds=(182,3844) /gb=NM_001682 /gi=4502286 /ug=Hs.78546 /len=4398	NM_001682	Hs.78546	NP_001673
425	7.47E-05	myeloid cell nuclear differentiation antigen (MNDA), mRNA /cds=(201,1424) /gb=NM_002432 /gi=4505226 /ug=Hs.153837 /len=1670	NM_002432	Hs.153837	NP_002423
459	0.000298	X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 3, mRNA /cds=(176,1180) /gb=NM_022550 /gi=12408648 /ug=Hs.150930 /len=1707	NM_022550	Hs.150930	NP_072044
465	0.000636	hypothetical protein, estradiol-induced (E2IG5), mRNA /cds=(71,643) /gb=NM_014367 /gi=21361426 /ug=Hs.5243 /len=1215	NM_014367	Hs.5243	NP_055182
525	0.000356	KDEL (Lys-Asp-Glu-Leu) containing 1 (KDELC1), mRNA /cds=(338,1846) /gb=NM_024089 /gi=13129085 /ug=Hs.44970 /len=2082	NM_024089	Hs.44970	NP_076994
700	8.5E-06	major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(65,829) /gb=NM_019111 /gi=18641378 /ug=Hs.409805 /len=1237	NM_019111	Hs.409805	NP_061984
731	5.82E-05	mitochondrial ribosomal protein S21 (MRPS21), transcript variant 2, nuclear gene encoding mitochondrial protein, mRNA /cds=(519,782) /gb=NM_018997 /gi=16950592 /ug=Hs.81281 /len=939	NM_018997	Hs.81281	NP_114107
793	0.000356	glyoxalase I (GLO1), mRNA /cds=(88,642) /gb=NM_006708 /gi=5729841 /ug=Hs.75207 /len=1993	NM_006708	Hs.75207	NP_006699
796	0.000948	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016	Hs.63525	NP_114366
852	0.001638	mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	AF224669		AAF35233.1
919	0.000117	putative protein tyrosine phosphatase (PTEN) mRNA, complete cds /cds=(1,1212) /gb=U93051 /gi=1916351 /ug=Hs.356062 /len=1212	U93051	Hs.356062	NP_000305
1039	5.44E-07	cDNA FLJ13779 fis, clone PLACE4000445, highly similar to mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212). /gb=AK023841 /gi=10435900 /ug=Hs.172069 /len=4959	AK023841	Hs.172069	T12506

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1064	2.57E-05	mitochondria solute carrier protein (MSCP)	AY032628		NP_061049
1113	0.001393	nischarin (NISCH), mRNA /cds=(27,4541) /gb=NM_007184 /gi=6005787 /ug=Hs.26285 /len=5132	NM_007184	Hs.26285	NP_009115
1134	0.000326	cDNA FLJ30093 fis, clone BNGH41000033. /gb=AK054655 /gi=16549241 /ug=Hs.349261 /len=2926	AK054655	Hs.349261	
1196	0.000492	FK506 binding protein 14, 22 kDa (FKBP14), mRNA /cds=(146,781) /gb=NM_017946 /gi=8923658 /ug=Hs.264636 /len=2248	NM_017946	Hs.264636	NP_060416
1241	0.000164	netrin 4 (NTN4), mRNA /cds=(452,2338) /gb=NM_021229 /gi=24475651 /ug=Hs.102541 /len=3607	NM_021229	Hs.102541	NP_067052
1259	4.15E-05	desmuslin (DMN), transcript variant A, mRNA /cds=(121,4818) /gb=NM_145728 /gi=22027637 /ug=Hs.10587 /len=7343	NM_145728	Hs.10587	NP_663780
1290	0.000959	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293	Hs.192102	NP_598411
1303	5.82E-05	imageqc_6_2001/snk86bdr81.y1 NIH_MGC_12 cDNA clone IMAGE:5110111 5', mRNA sequence /clone=IMAGE:5110111 /clone_end=5' /gb=BQ109159 /gi=20158813 /ug=Hs.433575 /len=604	BQ109159	Hs.433575	
1340	0.000326	structure specific recognition protein 1 (SSRP1), mRNA /cds=(275,2404) /gb=NM_003146 /gi=4507240 /ug=Hs.79162 /len=2839	NM_003146	Hs.79162	NP_003137
1581	0.000521	SH3 domain binding glutamic acid-rich protein like 3 (SH3BGR1), mRNA /cds=(72,353) /gb=NM_031286 /gi=13775197 /ug=Hs.109051 /len=764	NM_031286	Hs.109051	NP_112576
1673	2.76E-05	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
1804	0.000109	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPINE2), mRNA /cds=(210,1406) /gb=NM_006216 /gi=24307906 /ug=Hs.21858 /len=2129	NM_006216	Hs.21858	NP_006207

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
1813	0.000659	chromosome 14 open reading frame 80 (C14orf80), mRNA /cds=(330,1076) /gb=NM_173608 /gi=27734692 /ug=Hs.72363 /len=1419	NM_173608	Hs.72363	NP_775879
1843	0.000492	CDK2-associated protein 1 (CDK2AP1), mRNA /cds=(523,870) /gb=NM_004642 /gi=17978492 /ug=Hs.433201 /len=1627	NM_004642	Hs.433201	NP_004633
1946	4.31E-05	sphingolipid activator protein 1	J03015		NP_002769
1982	0.000356	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (ATP5G2), mRNA /cds=(60,485) /gb=NM_005176 /gi=6671590 /ug=Hs.89399 /len=746	NM_005176	Hs.89399	NP_005167
2013	4.31E-05	actinin, alpha 2 (ACTN2), mRNA /cds=(174,2858) /gb=NM_001103 /gi=4501892 /ug=Hs.83672 /len=4181	NM_001103	Hs.83672	NP_001094
2065	1.38E-05	tenascin C (hexabrachion) (TNC), mRNA /cds=(314,6919) /gb=NM_002160 /gi=4504548 /ug=Hs.289114 /len=7560	NM_002160	Hs.289114	NP_002151
2135	0.001538	hypothetical protein MDS025 (MDS025), mRNA /cds=(363,1127) /gb=NM_021825 /gi=21361605 /ug=Hs.154938 /len=1585	NM_021825	Hs.154938	NP_068597
2164	0.0012	KIAA1074 protein (KIAA1074), mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218	NP_055730
2340	0.001393	mRNA; cDNA DKFZp434F2311 (from clone DKFZp434F2311) /gb=AL137603 /gi=6808349 /ug=Hs.233890 /len=842	AL137603	Hs.233890	
2394	0.000164	RAN, member RAS oncogene family (RAN), mRNA /cds=(115,765) /gb=NM_006325 /gi=6042206 /ug=Hs.10842 /len=1656	NM_006325	Hs.10842	NP_006316
2418	5.82E-05	RAN binding protein 1 (RANBP1), low match	NM_002882		NP_002873
2434	0.000316	small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3), mRNA /cds=(88,468) /gb=NM_004175 /gi=4759159 /ug=Hs.1575 /len=626	NM_004175	Hs.1575	NP_004166
2490	0.000417	gonadotropin-releasing hormone receptor (GNRHR), mRNA /cds=(1749,2735) /gb=NM_000406 /gi=4504058 /ug=Hs.73064 /len=2735	NM_000406	Hs.73064	NP_000397
2584	0.000316	mRNA for KIAA0627 protein, partial cds. /cds=(1,3976) /gb=AB014527 /gi=3327067 /ug=Hs.108614 /len=5614	AB014527	Hs.108614	BAA31602.1
2748	0.00051	serologically defined colon cancer antigen 1 (SDCCAG1)	NM_004713		NP_004704

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2773	0.000326	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_139207	Hs.302649	NP_631946
2790	2.76E-05	choroideremia (Rab escort protein 1) (CHM), transcript variant 2950156, mRNA /cds=(31,1992) /gb=NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115	NM_000390	Hs.2010	NP_000381
2847	1.38E-05	lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2B, mRNA /cds=(138,1370) /gb=NM_013995 /gi=7669502 /ug=Hs.8262 /len=4006	NM_013995	Hs.8262	NP_054701
2912	0.000492	KIAA0690 protein (KIAA0690), mRNA /cds=(87,3980) /gb=NM_015179 /gi=15987120 /ug=Hs.60103 /len=4396	NM_015179	Hs.60103	NP_055994
2926	1.12E-06	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=NM_020414 /gi=14251213 /ug=Hs.155986 /len=2967	NM_020414	Hs.155986	NP_065147
3013	3.34E-06	uncharacterized hematopoietic stem/progenitor cells protein MDS031 (MDS031), mRNA /cds=(35,532) /gb=NM_018466 /gi=20070304 /ug=Hs.110853 /len=1358	NM_018466	Hs.110853	NP_060936
3017	0.0012	DC6 protein (DC6), mRNA /cds=(162,467) /gb=NM_020189 /gi=9910185 /ug=Hs.283740 /len=676	NM_020189	Hs.283740	NP_064574
3029	0.000927	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078	NM_020470	Hs.406422	NP_065203
3062	0.000117	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944	NM_006471	Hs.180224	NP_006462
3137	0.00121	yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452	H43642	Hs.418241	
3181	0.000521	protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740 /len=2661	NM_021131	Hs.400740	NP_821070
3185	3.07E-05	mRNA for repressor protein, partial cds. /cds=(1,2157) /gb=D30612 /gi=2723456 /ug=Hs.58167 /len=3737	D30612	Hs.58167	NP_003566

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3246	0.000295	UI-E-EJ0-ail-e-04-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ail-e-04-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ail-e-04-0-UI /clone_end=5' /gb=BM727687 /gi=19049020 /ug=Hs.446532 /len=1103	BM727687	Hs.446532	NP_079466.1
3266	0.000386	DKFZP564C186 protein (DKFZP564C186), mRNA /cds=(16,2265) /gb=NM_015658 /gi=7661605 /ug=Hs.134200 /len=2762	NM_015658	Hs.134200	NP_056473
3308	3.33E-05	putative breast adenocarcinoma marker (32kD) (BC-2), mRNA /cds=(130,798) /gb=NM_014453 /gi=7656921 /ug=Hs.12107 /len=903	NM_014453	Hs.12107	NP_055268
3321	0.000448	KIAA0097 gene product (KIAA0097), mRNA /cds=(27,5945) /gb=NM_014756 /gi=24307972 /ug=Hs.76989 /len=6449	NM_014756	Hs.76989	NP_055571
3331	0.001616	ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA /cds=(173,2794) /gb=NM_006208 /gi=13324676 /ug=Hs.11951 /len=3493	NM_006208	Hs.11951	NP_006199
3385	5.44E-07	SMC4 structural maintenance of chromosomes 4-like 1 (yeast) (SMC4L1), mRNA /cds=(233,4099) /gb=NM_005496 /gi=21361251 /ug=Hs.50758 /len=5261	NM_005496	Hs.50758	NP_005487
3396	3.64E-05	CGI-121 protein (CGI-121), mRNA /cds=(107,634) /gb=NM_016058 /gi=7705589 /ug=Hs.433212 /len=703	NM_016058	Hs.433212	NP_057142
3418	0.001449	syntaxin 4A (placental) (STX4A), mRNA /cds=(234,1127) /gb=NM_004604 /gi=20149559 /ug=Hs.83734 /len=1412	NM_004604	Hs.83734	NP_004595
3561	0.000636	Ikb kinase-b (IKK-beta) mRNA, complete cds /cds=(144,2414) /gb=AF080158 /gi=4185274 /ug=Hs.226573 /len=3058	AF080158	Hs.226573	AAD08997.1
3625	0.001021	UI-E-CQ1-aev-g-12-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aev-g-12-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aev-g-12-0-UI /clone_end=3' /gb=BM666437 /gi=18974127 /ug=Hs.279806 /len=1103	BM666437	Hs.279806	JC1087
3650	0.00143	hypothetical protein FLJ10326 (FLJ10326), mRNA /cds=(3,2297) /gb=NM_018060 /gi=8922355 /ug=Hs.262823 /len=3016	NM_018060	Hs.262823	NP_060530

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3685	0.001021	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA /cds=(122,1357) /gb=NM_003079 /gi=21264354 /ug=Hs.332848 /len=1576	NM_003079	Hs.332848	NP_003070
3686	3.07E-05	autism susceptibility candidate 2 (AUTS2), mRNA /cds=(322,4101) /gb=NM_015570 /gi=17864089 /ug=Hs.32168 /len=5972	NM_015570	Hs.32168	NP_056385
3701	0.000356	nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), mRNA /cds=(326,1378) /gb=NM_024047 /gi=20127621 /ug=Hs.301789 /len=1718	NM_024047	Hs.301789	NP_076952
3721	0.001393	apoptosis-associated speck-like protein containing a CARD (ASC), transcript variant 1, mRNA /cds=(241,828) /gb=NM_013258 /gi=22035618 /ug=Hs.71869 /len=936	NM_013258	Hs.71869	NP_660184
3731	0.000521	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
3792	1.38E-05	guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(333,1355) /gb=NM_002074 /gi=20357526 /ug=Hs.215595 /len=3147	NM_002074	Hs.215595	NP_002065
3903	0.000356	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA /cds=(367,1602) /gb=NM_003654 /gi=4502840 /ug=Hs.104576 /len=2415	NM_003654	Hs.104576	NP_003645
3941	0.000356	pinin, desmosome associated protein (PNN), mRNA /cds=(31,2262) /gb=NM_002687 /gi=4505922 /ug=Hs.44499 /len=2617	NM_002687	Hs.44499	NP_002678
4142	1.09E-05	chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643
4177	0.000356	connective tissue growth factor (CTGF), mRNA /cds=(146,1195) /gb=NM_001901 /gi=4503122 /ug=Hs.75511 /len=2312	NM_001901	Hs.75511	NP_001892
4209	7.4E-05	cDNA FLJ39491 fis, clone PROST2015924, weakly similar to Opa-interacting protein OIP2 mRNA. /gb=AK096810 /gi=21756383 /ug=Hs.274170 /len=2835	AK096810	Hs.274170	NP_852480

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4227	0.000298	ribosomal protein S15 (RPS15), mRNA /cds=(47,484) /gb=NM_001018 /gi=14591911 /ug=Hs.406683 /len=515	NM_001018	Hs.406683	NP_001009
4229	8.62E-05	chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717) /gb=NM_012073 /gi=24307938 /ug=Hs.1600 /len=1961	NM_012073	Hs.1600	NP_036205
4400	4.15E-05	mRNA; cDNA DKFZp762O1615 (from clone DKFZp762O1615) /gb=AL359558 /gi=8655613 /ug=Hs.284252 /len=2340	AL359558	Hs.284252	
4447	0.000521	runt-related transcription factor binding protein 2 (RUNXBP2), mRNA /cds=(394,6408) /gb=NM_006766 /gi=5803097 /ug=Hs.82210 /len=7869	NM_006766	Hs.82210	NP_006757
4631	1.38E-05	chemokine (C-X-C motif) ligand 9 (CXCL9), mRNA /cds=(40,417) /gb=NM_002416 /gi=4505186 /ug=Hs.77367 /len=2545	NM_002416	Hs.77367	NP_002407
4689	0.000659	t-complex-associated-testis-expressed 1-like (TCTE1L), mRNA /cds=(69,419) /gb=NM_006520 /gi=5730086 /ug=Hs.446392 /len=2156	NM_006520	Hs.446392	NP_006511
4770	0.000569	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
4845	0.000356	melanoma antigen, family D, 1 (MAGED1), mRNA /cds=(143,2479) /gb=NM_006986 /gi=14195633 /ug=Hs.5258 /len=2713	NM_006986	Hs.5258	NP_008917
4858	0.001393	AGENCOURT_8819408 NIH_MGC_18 cDNA clone IMAGE:6422878 5', mRNA sequence /clone=IMAGE:6422878 /clone_end=5' /gb=BQ941317 /gi=22356795 /ug=Hs.443078 /len=929	BQ941317	Hs.443078	
4927	0.000153	palmdelphin (PALMD), mRNA /cds=(286,1941) /gb=NM_017734 /gi=16306484 /ug=Hs.14606 /len=2581	NM_017734	Hs.14606	NP_060204
4975	2.54E-05	hypothetical protein MGC2747 (MGC2747), mRNA /cds=(93,248) /gb=NM_024104 /gi=13129111 /ug=Hs.194017 /len=1171	NM_024104	Hs.194017	NP_077009
5090	9.46E-06	U3 small nuclear RNA gene	M14061		
5117	2.76E-05	dynein, cytoplasmic, light polypeptide 1 (DNCL1), mRNA /cds=(94,363) /gb=NM_003746 /gi=4505812 /ug=Hs.5120 /len=643	NM_003746	Hs.5120	NP_003737



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5204	0.000882	stathmin-like 3 (STMN3), mRNA /cds=(83,625) /gb=NM_015894 /gi=14670374 /ug=Hs.285753 /len=2255	NM_015894	Hs.285753	NP_056978
5207	0.000746	v-maf musculoaponeurotic fibrosarcoma oncogene (avian) (MAF), mRNA /cds=(808,2019) /gb=NM_005360 /gi=5453735 /ug=Hs.30250 /len=2145	NM_005360	Hs.30250	NP_005351
5243	0.000326	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
5338	0.000356	thyroid hormone receptor interactor 3 (TRIP3), mRNA /cds=(39,506) /gb=NM_004773 /gi=22094078 /ug=Hs.2210 /len=950	NM_004773	Hs.2210	NP_004764
5383	0.001449	ADP-ribosylation factor GTPase activating protein 3 (ARFGAP3), mRNA /cds=(39,1589) /gb=NM_014570 /gi=20070254 /ug=Hs.13014 /len=2666	NM_014570	Hs.13014	NP_055385
5396	0.000951	Hypothetical protein(cDNA: FLJ23122 fis, clone LNG08008)	AK026775		NP_003608
5411	0.000569	DKFZp566J2446 (from clone DKFZp566J2446)	AL050082		NP_008944
5653	2.57E-05	glypican 3 (GPC3), mRNA /cds=(191,1933) /gb=NM_004484 /gi=5360213 /ug=Hs.119651 /len=2382	NM_004484	Hs.119651	NP_004475
5654	0.000882	Tis11d	U07802		AAA91778.1
5767	2.61E-05	hypothetical gene supported by AL449243 (LOC91689), mRNA /cds=(80,403) /gb=NM_033318 /gi=21314768 /ug=Hs.306083 /len=1586	NM_033318	Hs.306083	NP_201575
5810	3.64E-05	non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA /cds=(73,531) /gb=NM_002512 /gi=4505408 /ug=Hs.433416 /len=670	NM_002512	Hs.433416	NP_002503
5826	0.001616	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
5941	8.5E-06	ubiquitin-protein isopeptide ligase (E3) (KIAA0010), mRNA /cds=(304,3555) /gb=NM_014671 /gi=7661855 /ug=Hs.155287 /len=5160	NM_014671	Hs.155287	NP_055486
6027	0.000356	mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA /cds=(182,1093) /gb=NM_005924 /gi=21396478 /ug=Hs.77858 /len=2284	NM_005924	Hs.77858	NP_005915

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
6046	0.000711	KIAA0092 gene product (KIAA0092), mRNA /cds=(54,1478) /gb=NM_014679 /gi=7661899 /ug=Hs.151791 /len=2913	NM_014679	Hs.151791	NP_055494
6202	0.000492	Si-1-8-16 mRNA, partial cds	AB044752		NP_061130
6360	0.000711	heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), transcript variant 1, mRNA /cds=(581,1843) /gb=NM_005463 /gi=14110410 /ug=Hs.372673 /len=3514	NM_005463	Hs.372673	NP_112740
6458	9.46E-06	mitochondrion, complete genome	NC_001807		
6491	0.001393	RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, mRNA /cds=(472,2421) /gb=NM_002907 /gi=14591903 /ug=Hs.235069 /len=2866	NM_002907	Hs.235069	NP_116559
6510	0.001449	UI-H-DT0-atx-f-13-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865612 3', mRNA sequence /clone=IMAGE:5865612 /clone_end=3' /gb=BM994157 /gi=19719058 /ug=Hs.406666 /len=1283	BM994157	Hs.406666	
6526	0.001021	sequestosome 1 (SQSTM1), mRNA /cds=(41,1363) /gb=NM_003900 /gi=19923742 /ug=Hs.182248 /len=2870	NM_003900	Hs.182248	NP_003891
6595	8.62E-05	H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=NM_000186 /gi=4504374 /ug=Hs.250651 /len=3926	NM_000186	Hs.250651	NP_000177
6622	0.000669	aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 /len=1662	NM_000385	Hs.76152	NP_000376
6663	0.000298	PRO0461 protein (PRO0461), mRNA /gb=NM_031268 /gi=20588827 /ug=Hs.25063 /len=1100	NM_031268	Hs.25063	Q9UI25
6733	1.38E-05	putative transmembrane protein (NMA), mRNA /cds=(373,1155) /gb=NM_012342 /gi=6912533 /ug=Hs.78776 /len=1521	NM_012342	Hs.78776	NP_036474
6901	0.000983	cDNA FLJ34353 fis, clone FEBRA2011665. /cds=(178,573) /gb=AK091672 /gi=21750096 /ug=Hs.13477 /len=3517	AK091672	Hs.13477	BAC03718.1
6925	0.000298	mitochondrial ribosomal protein S22 (MRPS22), nuclear gene encoding mitochondrial protein, mRNA /cds=(9,1091) /gb=NM_020191 /gi=16554602 /ug=Hs.107127 /len=1155	NM_020191	Hs.107127	NP_064576

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
6962	2.03E-05	hypothetical protein FLJ10377 (FLJ10377), mRNA /cds=(116,2395) /gb=NM_018077 /gi=8922387 /ug=Hs.274263 /len=2809	NM_018077	Hs.274263	NP_060547
6999	0.000298	ring finger protein 20 (RNF20), mRNA /cds=(91,3018) /gb=NM_019592 /gi=16554452 /ug=Hs.168095 /len=3936	NM_019592	Hs.168095	NP_062538
7030	1.38E-05	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304	NM_004355	Hs.84298	NP_004346
7142	0.001116	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
7287	0.000492	mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054 /ug=Hs.94030 /len=1341	AL110152	Hs.94030	
7382	0.000316	cortactin binding protein 2 (CORTBP2), mRNA /cds=(93,5084) /gb=NM_033427 /gi=16975495 /ug=Hs.293539 /len=5975	NM_033427	Hs.293539	NP_219499
7398	0.000463	laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA /cds=(50,9382) /gb=NM_000426 /gi=4557708 /ug=Hs.75279 /len=9534	NM_000426	Hs.75279	NP_000417
7420	0.001021	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(32,1711) /gb=NM_020474 /gi=13124890 /ug=Hs.80120 /len=3778	NM_020474	Hs.80120	NP_065207
7556	0.000173	interleukin enhancer binding factor 1 (ILF1), mRNA /cds=(198,2165) /gb=NM_004514 /gi=4758599 /ug=Hs.296281 /len=3059	NM_004514	Hs.296281	NP_852096
7725	8.5E-06	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=NM_002794 /gi=22538463 /ug=Hs.432607 /len=850	NM_002794	Hs.432607	NP_002785
7899	0.000117	UI-E-DW0-agk-i-01-0-UI.r1 UI-E-DW0 cDNA clone UI-E-DW0-agk-i-01-0-UI 5', mRNA sequence /clone=UI-E-DW0-agk-i-01-0-UI /clone_end=5' /gb=BM696546 /gi=19009804 /ug=Hs.356149 /len=1200	BM696546	Hs.356149	
7906	0.001071	cDNA FLJ30587 fis, clone BRAWH2007800, weakly similar to Ovo protein. /gb=AK055149 /gi=16549814 /ug=Hs.367639 /len=2529	AK055149	Hs.367639	

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
7915	4.31E-05	GK001 protein (GK001), mRNA /cds=(185,1636) /gb=NM_020198 /gi=9910241 /ug=Hs.8207 /len=3294	NM_020198	Hs.8207	NP_064583
7927	0.0003	UI-H-EZ1-bca-n-05-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1- bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083	BQ774356	Hs.43227	
7947	3.9E-07	EST (AV690707 GKC H.sapiens cDNA	AV690707		NP_004577
7952	0.000793	EST (AI683276 tx02h12.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2268071 3')	AI683276		
8043	0.000173	hypothetical protein from BCRA2 region (CG005), mRNA /cds=(166,1917) /gb=NM_014887 /gi=7656970 /ug=Hs.23518 /len=2825	NM_014887	Hs.23518	NP_055702
8069	0.001021	Similar to nuclear localization signals binding protein 1, clone MGC:21810 IMAGE:4183576, mRNA, complete cds /cds=(58,375) /gb=BC016981 /gi=16877469 /ug=Hs.244624 /len=2059	BC016981	Hs.244624	AAH16981.1
8134	0.000104	CGI-204 mRNA, complete cds. /cds=(41,799) /gb=AF285120 /gi=9858830 /ug=Hs.283734 /len=2865	AF285120	Hs.283734	NP_817125
8179	0.000364	karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271 /gi=24797085 /ug=Hs.113503 /len=5977	NM_002271	Hs.113503	NP_002262
8202	0.000364	transcription factor Dp-1 (TFDP1), mRNA /cds=(222,1454) /gb=NM_007111 /gi=21361419 /ug=Hs.79353 /len=2394	NM_007111	Hs.79353	NP_009042
8315	0.000448	UI-H-ED0-awz-g-17-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825704 3', mRNA sequence /clone=IMAGE:5825704 /clone_end=3' /gb=BM994952 /gi=19719853 /ug=Hs.15702 /len=1200	BM994952	Hs.15702	
8334	0.000272	EST (MR4-ST0070-051099-009-e09 ST0070)	AW387240		NP_036546
8351	0.000806	EST zr46h01.s1 Soares NhHMPu S1 cDNA clone 666481 3'	AA233076		
8360	0.000521	EST(zf51h11.r1 Soares retina N2b4HR clone IMAGE:380517 5' contains MER17.b2 MER17 repeat)	AA044938		
8466	0.000625	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	AAM28436.1

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
8580	0.001546	BX096173 Soares_testis_NHT cDNA clone IMAGp998F151793, mRNA sequence /clone=IMAGp998F151793_/_IMAGE:730766 /gb=BX096173 /gi=27842669 /ug=Hs.188780 /len=556	BX096173	Hs.188780	
8622	0.001393	FLJ30623 fis, clone CTONG2001748 /cds=UNKNOWN /gb=AK055185 /gi=16549855 /ug=Hs.351574 /len=2870	AK055185	Hs.351574	NP_079050
8663	0.000326	hypothetical protein BC018453 (LOC129531), mRNA /cds=(49,798) /gb=NM_138798 /gi=20270348 /ug=Hs.14222 /len=963	NM_138798	Hs.14222	NP_620153
8706	0.000164	cDNA FLJ31306 fis, clone LIVER1000111. /gb=AK055868 /gi=16550703 /ug=Hs.442335 /len=2360	AK055868	Hs.442335	NP_071431.1
8717	8.5E-06	EST(cDNA clone IMAGE:2622241 3' )	AW131141		NP_055262
8770	0.000173	UI-H-DF0-bey-f-20-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bey-f-20-0-UI 3', mRNA sequence /clone=UI-H-DF0-bey-f-20-0-UI /clone_end=3' /gb=CA427170 /gi=24789896 /ug=Hs.27996 /len=1082	CA427170	Hs.27996	
8771	0.000298	mitochondrion, complete genome	NC_001807		
8804	4.31E-05	E2F transcription factor 5, p130-binding (E2F5), mRNA /cds=(35,1075) /gb=NM_001951 /gi=12669916 /ug=Hs.2331 /len=1752	NM_001951	Hs.2331	NP_001942
8843	3.07E-05	No significant match, ORF-1(69~499)low complexity			
8853	0.000153	No significant match (ORF:+1:13~144[132], +2:50~151[102])			
8856	0.000625	control			
8862	0.000326	cDNA FLJ14368 fis, clone HEMBA1001122. /gb=AK027274 /gi=14041848 /ug=Hs.330716 /len=1543	AK027274	Hs.330716	
8865	3.07E-05	cDNA FLJ12091 fis, clone HEMBB1002582	AK022153		
8875	0.000326	No significant match, ORF+2(131~292)			
8951	0.000569	PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA /cds=(231,3389) /gb=NM_153831 /gi=27886591 /ug=Hs.740 /len=4453	NM_153831	Hs.740	NP_722560
9026	0.000105	df118f01.w1 Morton Fetal Cochlea cDNA clone IMAGE:2539897 3', mRNA sequence /clone=IMAGE:2539897 /clone_end=3' /gb=BI495496 /gi=15334840 /ug=Hs.345508 /len=553	BI495496	Hs.345508	

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
9065	0.000983	UI-H-BI0p-abb-b-05-0-UI.s1 NCI_CGAP_Sub2 cDNA clone IMAGE:2711001 3', mRNA sequence /clone=IMAGE:2711001 /clone_end=3' /gb=AW015262 /gi=5863949 /ug=Hs.440665 /len=854	AW015262	Hs.440665	
9078	0.000959	cDNA FLJ13207 fis, clone NT2RP4000023. /gb=AK023269 /gi=10435128 /ug=Hs.14355 /len=2633	AK023269	Hs.14355	
9142	0.000492	cDNA FLJ38449 fis, clone FEBRA2019389. /gb=AK095768 /gi=21755098 /ug=Hs.146312 /len=2628	AK095768	Hs.146312	NP_071431.1
9161	2.07E-05	cDNA FLJ31107 fis, clone IMR322000152. /gb=AK055669 /gi=16550452 /ug=Hs.405954 /len=2250	AK055669	Hs.405954	
9271	2.8E-05	fj53d02.x1 adult brain Danio rerio cDNA 3' similar to SW:EF2_CHICK Q90705 ELONGATION FACTOR 2 ;	AW281691		EFHU2
9364	8.5E-06	FLJ12419 fis, clone MAMMA1003047, highly similar to Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA /cds=UNKNOWN /gb=AK022481 /gi=10433892 /ug=Hs.105779 /len=3054	AK022481	Hs.105779	NP_056981
9376	0.000928	tenascin XB (TNXB), transcript variant XB, mRNA /cds=(205,13074) /gb=NM_019105 /gi=20544188 /ug=Hs.169886 /len=13268	NM_019105	Hs.169886	NP_115859
9451	5.82E-05	phospholipase A2-activating protein (PLAA), mRNA /cds=(29,2245) /gb=NM_004253 /gi=21361288 /ug=Hs.27182 /len=3240	NM_004253	Hs.27182	NP_004244
9463	0.000521	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
9488	3.07E-05	UDP-N-actetylglucosamine pyrophosphorylase 1 (UAP1), mRNA /cds=(312,1829) /gb=NM_003115 /gi=19923738 /ug=Hs.21293 /len=2332	NM_003115	Hs.21293	NP_003106
9535	0.001449	Hypothetical protein 669, cDNA FLJ32614 fis, clone STOMA2000121, moderately similar to Fugu rubripes CCBL1 gene (AK057176.1) (=CG6950 gene, BC000819.1)	BC000819	Hs.180378	NP_062556
9573	0.000326	cDNA FLJ39084 fis, clone NT2RP7018871. /cds=(491,1024) /gb=AK096403 /gi=21755888 /ug=Hs.356835 /len=2242	AK096403	Hs.356835	BAC04779.1

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
9633	0.000298	U7 snRNP-specific Sm-like protein LSM10 (LSM10), mRNA /cds=(151,522) /gb=NM_032881 /gi=14249631 /ug=Hs.3496 /len=869	NM_032881	Hs.3496	NP_116270
9634	4.31E-05	cDNA PSEC0070 fis, clone NT2RP2001508, moderately similar to OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT. /cds=(94,954) /gb=AK075380 /gi=22761428 /ug=Hs.183454 /len=2510	AK075380	Hs.183454	NP_849193
9771	0.000521	EST(oo43e04.s1 NCI_CGAP_Lu5 clone IMAGE:1568958 3' contains L1.t1 L1 repeat)	AA973377		
9862	0.001393	component of oligomeric golgi complex 1 (COG1), mRNA /cds=(27,2969) /gb=NM_018714 /gi=21237782 /ug=Hs.283109 /len=3047	NM_018714	Hs.283109	NP_061184
9895	4.31E-05	FLJ23227 fis, clone CAE00645, highly similar to AF052138 Homo sapiens clone 23718 mRNA sequence /cds=UNKNOWN /gb=AK026880 /gi=10439841 /ug=Hs.6580 /len=1729	AK026880	Hs.6580	NP_031397.1
9975	0.000298	RAB6A, member RAS oncogene family (RAB6A), mRNA /cds=(427,1053) /gb=NM_002869 /gi=19923230 /ug=Hs.5636 /len=3079	NM_002869	Hs.5636	NP_002860
9995	0.000659	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3 (B3GALT3), transcript variant 1, mRNA /cds=(399,1394) /gb=NM_003781 /gi=15451873 /ug=Hs.267695 /len=3210	NM_003781	Hs.267695	NP_149359
9998	3.07E-05	chromosome 20 open reading frame 14 (C20orf14), mRNA /cds=(100,2925) /gb=NM_012469 /gi=6912731 /ug=Hs.31334 /len=3060	NM_012469	Hs.31334	NP_036601
10021	3.07E-05	RaiGDS-like gene (RGL), mRNA /cds=(450,2861) /gb=NM_015149 /gi=20127535 /ug=Hs.79219 /len=5111	NM_015149	Hs.79219	NP_055964
10024	1.38E-05	DnaJ (Hsp40) subfamily B, member 11 (DNAJB11), mRNA /cds=(160,1236) /gb=NM_016306 /gi=25014110 /ug=Hs.278605 /len=1621	NM_016306	Hs.278605	NP_057390
10044	2.76E-05	ER-resident protein ERdj5 (ERdj5), mRNA /cds=(416,2797) /gb=NM_018981 /gi=24308126 /ug=Hs.1098 /len=4193	NM_018981	Hs.1098	NP_061854

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
10050	0.000164	FLJ10765 fis, clone NT2RP4000111, highly similar to CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT /cds=UNKNOWN /gb=AK001627 /gi=7022996 /ug=Hs.224961 /len=4352	AK001627	Hs.224961	
10061	5.82E-05	UI-H-EU0-azv-c-01-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5854008 3', mRNA sequence /clone=IMAGE:_5854008 /clone_end=3' /gb=BQ181694 /gi=20357186 /ug=Hs.177936 /len=1076	BQ181694	Hs.177936	
10069	5.82E-05	hypothetical protein FLJ20297 (FLJ20297), mRNA /cds=(111,2507) /gb=NM_017751 /gi=8923276 /ug=Hs.94491 /len=3682	NM_017751	Hs.94491	NP_060421
10087	2.07E-05	cDNA FLJ30064 fis, clone ADRGL2000323. /cds=(118,516) /gb=AK054626 /gi=16549205 /ug=Hs.188504 /len=2081	AK054626	Hs.188504	BAB70777.1
10094	8.88E-06	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2(NFKBIL2), mRNA /cds=(473,4132) /gb=NM_013432/gi=15718771 /ug=Hs.323834 /len=4501	NM_013432	Hs.323834	NP_038460
10099	0.000711	intersectin (ITSN) gene, exons and short form, partial cds	AF064245		AAC80436.1
10105	2.76E-05	programmed cell death 2 (PDCD2), transcript variant 2, mRNA /cds=(80,766) /gb=NM_144781 /gi=21735593 /ug=Hs.367900 /len=2066	NM_144781	Hs.367900	NP_659005
10126	0.000356	mRNA for KIAA0647 protein, partial cds /cds=UNKNOWN /gb=AB014547 /gi=20521118 /ug=Hs.141727 /len=5719	AB014547	Hs.141727	NP_004678
10163	1.46E-05	KIAA0062 mRNA, partial cds /cds=(1,1598) /gb=D31887 /gi=505101 /ug=Hs.89868 /len=4573	D31887	Hs.89868	BAA06685.1
10183	5.82E-05	cDNA: FLJ20924 fis, clone ADSE00928. /gb=AK024577 /gi=10436889 /ug=Hs.306692 /len=1516	AK024577	Hs.306692	JC5238
10228	0.001449	hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=NM_018064 /gi=14149717 /ug=Hs.101514 /len=1506	NM_018064	Hs.101514	NP_060534
10236	0.000882	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
10302	0.000427	EST CM4-CT0343-301199-052-d11 CT0343	AW363671		NP_000998



Spot	p-value	Description	Accession	Unigene	Protein Accession No.
10348	0.000523	BX103634 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGp998O213969, mRNA sequence /clone=IMAGp998O213969;_IMAGE:156 6572 /gb=BX103634 /gi=27845812 /ug=Hs.134848 /len=554	BX103634	Hs.134848	
10428	0.000694	clone IMAGE:5275048, mRNA /gb=BC041379 /gi=27552809 /ug=Hs.187646 /len=3258	BC041379	Hs.187646	
10479	3.07E-05	UI-H-BI4-aos-c-04-0-UI.s1 NCI_CGAP_Sub8 cDNA clone IMAGE:3085830 3', mRNA sequence /clone=IMAGE:3085830 /clone_end=3' /gb=BF508907 /gi=11592205 /ug=Hs.433695 /len=932	BF508907	Hs.433695	NP_003874.2
10484	3.64E-05	hypothetical protein FLJ20255 (FLJ20255), mRNA /cds=(146,1090) /gb=NM_017728 /gi=8923229 /ug=Hs.15797 /len=1769	NM_017728	Hs.15797	NP_060198
10501	2.76E-05	UI-E-DW0-agg-d-24-0-UI.r1 UI-E-DW0 cDNA clone UI-E-DW0-agg-d-24-0-UI 5', mRNA sequence /clone=UI-E-DW0-agg-d- 24-0-UI /clone_end=5' /gb=BM706154 /gi=19019412 /ug=Hs.433446 /len=1003	BM706154	Hs.433446	P51003
10528	0.000104	FLJ32238 fis, clone PLACE6004993 /cds=UNKNOWN /gb=AK056800 /gi=16552307 /ug=Hs.183161 /len=2204	AK056800	Hs.183161	NP_036595
10533	5.82E-05	EST(Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA 5' )	BI964140		NP_006531
10594	0.000791	UI-H-EZ1-bbh-j-15-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1- bbh-j-15-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbh-j-15-0-UI /clone_end=3' /gb=BQ575990 /gi=21479307 /ug=Hs.445509 /len=1032	BQ575990	Hs.445509	
10606	0.001387	EST(fp43g05.x1 zebrafish gridded kidney Danio rerio cDNA clone 4759496 3' similar to contains element MER21 repetitive element ;)	BG891931		
10657	1.01E-05	cDNA FLJ34771 fis, clone NT2NE2003150. /gb=AK092090 /gi=21750599 /ug=Hs.433010 /len=2424	AK092090	Hs.433010	NP_060312.1
10684	3.64E-05	EST(cDNA clone IMAGE:4090855 3' )	BF447403		NP_002806
10783	0.000298	EST (nm30c04.s1 NCI_CGAP_Lip2 IMAGE:1061670)	AA569171		
10786	0.001289	EST (MR0-SN0040-060400-001-h09 SN0040)	AW867719		
10864	0.000492	EST (ab81d11.s1 Stratagene fetal retina 937202 IMAGE:853365 3')	AA663308		

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
10967	0.000681	cDNA /clone=cD622 /gb=AF107454 /gi=5052209 /ug=Hs.107537 /len=4850	AF107454	Hs.107537	NP_071903
11107	8.5E-06	cDNA FLJ11041 fis, clone PLACE1004405. /gb=AK001903 /gi=7023457 /ug=Hs.28792 /len=1932	AK001903	Hs.28792	
11139	0.000298	ESTs, cDNA, 3' end /clone=IMAGE:3676432 /clone_end=3' /gb=BF593483 /gi=11685729 /ug=Hs.235860 /len=582	BF593483	Hs.235860	Q9H334
11183	0.000298	No significant match			
11276	1.38E-05	FLN29 gene product (FLN29), mRNA /cds=(55,1803) /gb=NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618	NM_006700	Hs.5148	NP_006691
11279	0.000298	cDNA FLJ11660 fis, clone HEMBA1004610. /gb=AK021722 /gi=10432962 /ug=Hs.281895 /len=1769	AK021722	Hs.281895	
11323	0.001393	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB), mRNA	XM_032491		
11345	0.000719	HT001 protein (HT001), mRNA /cds=(242,1204) /gb=NM_014065 /gi=7661837 /ug=Hs.279040 /len=1402	NM_014065	Hs.279040	NP_054784
11357	3.07E-05	splicing factor 3a, subunit 1, 120kDa (SF3A1), mRNA /cds=(132,2513) /gb=NM_005877 /gi=20127483 /ug=Hs.406277 /len=2944	NM_005877	Hs.406277	NP_005868
11414	1.38E-05	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635	Hs.78713	NP_005879
11462	3.07E-05	ta10c07.x1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:2043660 3', mRNA sequence /clone=IMAGE:2043660 /clone_end=3' /gb=AI581285 /gi=4565661 /ug=Hs.309697 /len=467	AI581285	Hs.309697	
11595	0.000173	hypothetical protein FLJ22104 (FLJ22104), mRNA /cds=(63,1127) /gb=NM_022918 /gi=12597666 /ug=Hs.183887 /len=2952	NM_022918	Hs.183887	NP_075069
11684	0.001001	cDNA: FLJ21311 fis, clone COL02167. /gb=AK024964 /gi=10437390 /ug=Hs.173933 /len=3216	AK024964	Hs.173933	NP_005586
11688	0.000173	hypothetical protein from clone 24796 (LOC57146), mRNA /cds=(113,598) /gb=NM_020422 /gi=21361853 /ug=Hs.27191 /len=1683	NM_020422	Hs.27191	NP_065155

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
11693	0.001001	cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA /cds=(1,3723) /gb=NM_016952 /gi=8393083 /ug=Hs.159565 /len=3986	NM_016952	Hs.159565	NP_058648
11751	3.07E-05	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA /cds=(151,510) /gb=NM_004549 /gi=19923255 /ug=Hs.193313 /len=2168	NM_004549	Hs.193313	NP_004540
11807	0.000681	peptidylprolyl isomerase (cyclophilin)-like 1 (PPIL1), mRNA /cds=(222,722) /gb=NM_016059 /gi=22035675 /ug=Hs.27693 /len=1723	NM_016059	Hs.27693	NP_057143
11834	0.000274	hypothetical protein LOC93550 (LOC93550), mRNA /cds=(217,2400) /gb=NM_174890 /gi=28376663 /ug=Hs.377945 /len=3256	NM_174890	Hs.377945	NP_777550
11909	3.07E-05	HRD1 protein (HRD1), transcript variant 2, mRNA /cds=(95,1948) /gb=NM_172230 /gi=27436926 /ug=Hs.334819 /len=3074	NM_172230	Hs.334819	NP_757385
11912	9.46E-06	hypothetical protein MGC40157 (MGC40157), mRNA /cds=(106,498) /gb=NM_152350 /gi=22748758 /ug=Hs.295362 /len=1250	NM_152350	Hs.295362	NP_689563
11939	1.38E-05	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
11962	8.88E-06	aquaporin 3 (AQP3), mRNA /cds=(63,941) /gb=NM_004925 /gi=22165421 /ug=Hs.234642 /len=1835	NM_004925	Hs.234642	NP_004916
12005	0.000153	EST(no44e03.s1 NCI_CGAP_Pr23 cDNA clone IMAGE:1103548)	AA622352		
12037	2.07E-05	EST(EST58819 Infant brain 3' contains Alu repeat)	AA351153		
12056	4.31E-05	EST(ak48e09.s1 Soares testis NHT clone IMAGE:1409224 3')	AA860225		
12112	0.000326	EST(xu58f03.x1 NCI_CGAP_Ut1 clone IMAGE:2805917 3' TR:O35371 O35371 PERIPHERAL BENZODIAZEPINE RECEPTOR ASSOCIATED PROTEIN)	AW511419		NP_073572
12182	0.000328	Williams-Beuren Syndrome critical region protein 20 copy B (WBSCR20B), mRNA /cds=(984,1448) /gb=NM_145645 /gi=21717802 /ug=Hs.406306 /len=1634	NM_145645	Hs.406306	NP_663620

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
12261	0.001021	UI-E-EO1-aid-o-06-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aid-o-06-0-UI 3', mRNA sequence /clone=UI-E-EO1-aid-o-06-0-UI /clone_end=3' /gb=BM677516 /gi=18987412 /ug=Hs.443680 /len=1044	BM677516	Hs.443680	
12383	0.000356	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence	NC_001144		
12390	3.07E-05	UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445	BQ017647	Hs.124747	
12426	0.000636	602590145F1 NIH_MGC_76 cDNA clone IMAGE:4724074 5', mRNA sequence /clone=IMAGE:4724074 /clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792	BG564169	Hs.444093	
12477	0.000117	602022714F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4158098 5', mRNA sequence /clone=IMAGE:4158098 /clone_end=5' /gb=BF347758 /gi=11295353 /ug=Hs.280146 /len=738	BF347758	Hs.280146	
12512	0.000158	nx84b05.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:1268913 3', mRNA sequence /clone=IMAGE:1268913 /clone_end=3' /gb=AA720890 /gi=2737025 /ug=Hs.291473 /len=268	AA720890	Hs.291473	
12515	0.000158	stress 70 protein chaperone, microsome-associated, 60kDa (STCH), mRNA /cds=(37,1452) /gb=NM_006948 /gi=24431965 /ug=Hs.352341 /len=3998	NM_006948	Hs.352341	NP_008879
12544	0.001164	cDNA FLJ33247 fis, clone ASTRO2004974. /gb=AK090566 /gi=21748752 /ug=Hs.349938 /len=3175	AK090566	Hs.349938	NP_076936.1
12583	0.000326	Novel, ORF+3(45~300)			
12603	0.001116	BX094154 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998P17654, mRNA sequence /clone=IMAGp998P17654_/_IMAGE:293632 /gb=BX094154 /gi=27826950 /ug=Hs.12962 /len=758	BX094154	Hs.12962	
12608	8.81E-05	mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081) /gb=AL080234 /gi=5262727 /ug=Hs.432862 /len=2159	AL080234	Hs.432862	NP_060312.1
12615	0.000153	No significant match, low complexity			
12794	0.001443	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
12835	3.64E-05	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
12880	1.38E-05	EST(cDNA clone IMAGE:1470581 3' )	AA873731		NP_004087
12901	0.000659	ESTs, cDNA /clone=IMAGE:1203867 /gb=AA640737 /gi=2565987 /ug=Hs.336767 /len=416	AA640737	Hs.336767	
12918	0.000295	cDNA: FLJ21962 fis, clone HEP05564. /gb=AK025615 /gi=10438186 /ug=Hs.7567 /len=3323	AK025615	Hs.7567	
12952	3.07E-05	cDNA: FLJ21265 fis, clone COL01584. /gb=AK024918 /gi=10437333 /ug=Hs.306728 /len=2233	AK024918	Hs.306728	
12981	6.97E-05	selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834	NM_170746	Hs.290874	NP_734467
13047	0.000295	novel			
13058	5.82E-05	No significant match, ORF+1(1~237),- 3(47~832)			
13064	1.38E-05	No significant match (ORF:- 1:37~186[150])			
13095	0.000316	No significant match, ORF-3(30~198)			
13197	0.000298	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
13230	0.000295	ATP-binding cassette, sub-family E (OABP), member 1 (ABCE1), mRNA /cds=(118,1917) /gb=NM_002940 /gi=4506558 /ug=Hs.12013 /len=3568	NM_002940	Hs.12013	NP_002931
13330	0.001164	bridging integrator 2 (BIN2), mRNA /cds=(39,1736) /gb=NM_016293 /gi=7706486 /ug=Hs.14770 /len=2206	NM_016293	Hs.14770	NP_057377
13338	0.000523	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902 /gi=20070322 /ug=Hs.129445 /len=2952	NM_022902	Hs.129445	NP_076960
13364	8.5E-06	hypothetical protein BC009518 (LOC90799), mRNA /cds=(59,2524) /gb=NM_138363 /gi=19923898 /ug=Hs.135265 /len=2705	NM_138363	Hs.135265	NP_612372
13512	0.000928	EST EST384986 MAGE resequences, MAGL	AW972891		NP_078939

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
13761	6.73E-05	optic atrophy 1 (autosomal dominant) (OPA1), nuclear gene encoding mitochondrial protein, transcript variant 8, mRNA /cds=(56,3103) /gb=NM_130837 /gi=18860844 /ug=Hs.147946 /len=6029	NM_130837	Hs.147946	NP_570850
13789	0.000357	cDNA FLJ31372 fis, clone NB9N42000281. /gb=AK055934 /gi=16550786 /ug=Hs.89388 /len=2606	AK055934	Hs.89388	
13812	0.001554	plasminogen activator, tissue (PLAT), transcript variant 1, mRNA /cds=(209,1897) /gb=NM_000930 /gi=14702165 /ug=Hs.274404 /len=2653	NM_000930	Hs.274404	NP_127509
13818	3.07E-05	bladder cancer-related protein (LHX) gene, partial 3'UTR sequence	AY034106		NP_002856
13854	3.07E-05	palmdelphin (PALMD), mRNA /cds=(286,1941) /gb=NM_017734 /gi=16306484 /ug=Hs.14606 /len=2581	NM_017734	Hs.14606	NP_060204
13863	0.001021	cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BTF3. /cds=(91,567) /gb=AK027750 /gi=14042660 /ug=Hs.93748 /len=2203	AK027750	Hs.93748	BAB55342.1
13869	0.00135	peptidylprolyl isomerase C (cyclophilin C) (PPIC), mRNA /cds=(88,726) /gb=NM_000943 /gi=20149506 /ug=Hs.110364 /len=1015	NM_000943	Hs.110364	NP_000934
13903	0.000791	cDNA FLJ32300 fis, clone PROST2002227, highly similar to M-PHASE PHOSPHOPROTEIN 10. /gb=AK056862 /gi=16552379 /ug=Hs.201676 /len=2334	AK056862	Hs.201676	NP_005782
13954	0.000492	EST nw48e08.s1 NCI_CGAP_Ew1 IMAGE:1249862	AA730589		
14039	9.46E-06	hypothetical protein FLJ10038 (FLJ10038), mRNA /cds=(167,577) /gb=NM_017976 /gi=8922197 /ug=Hs.181202 /len=1461	NM_017976	Hs.181202	NP_060446
14081	0.000316	mRNA; cDNA DKFZp434H2019 (from clone DKFZp434H2019) /gb=AL137535 /gi=6808211 /ug=Hs.15806 /len=1974	AL137535	Hs.15806	NP_116212.1
14094	0.000112	EST (wh67d04.x1 NCI_CGAP_Kid11 IMAGE:2385799 3')	AI766049		T08781
14166	0.001443	cDNA FLJ38536 fis, clone HCHON2001200. /gb=AK095855 /gi=21755199 /ug=Hs.30089 /len=2950	AK095855	Hs.30089	
14247	2.76E-05	clone IMAGE:4836898, mRNA /gb=BC042527 /gi=27502923 /ug=Hs.434231 /len=2935	BC042527	Hs.434231	

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
14291	0.000377	calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734
14371	0.000356	EST391381 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW979271 /gi=8170559 /ug=Hs.293184 /len=577	AW979271	Hs.293184	
14399	3.37E-06	EST, clone 25032 mRNA sequence /cds=UNKNOWN /gb=AF131764 /gi=4406586 /ug=Hs.13399 /len=1798	AF131764	Hs.396998	NP_071919
14427	0.000463	EST(cDNA clone IMAGE:2420325 3' )	AI814793		NP_005617
14455	0.001532	No significant match, ORF+3(135~404)			
14501	0.000716	No significant match			
14517	0.000295	xq09e02.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2750138 3' similar to contains Alu repetitive element;; mRNA sequence /clone=IMAGE:2750138 /clone_end=3' /gb=AW517395 /gi=7155477 /ug=Hs.445194 /len=519	AW517395	Hs.445194	NP_064622.1
14626	0.000949	cDNA FLJ31439 fis, clone NT2NE2000707. /gb=AK056001 /gi=16550873 /ug=Hs.349656 /len=2009	AK056001	Hs.349656	NP_060312.1
14784	0.000882	ak04g10.s1 Soares_parathyroid_tumor_NbHPA cDNA clone IMAGE:1405026 3' similar to contains Alu repetitive element;; mRNA sequence /clone=IMAGE:1405026 /clone_end=3' /gb=AA845596 /gi=2933355 /ug=Hs.275849 /len=525	AA845596	Hs.275849	NP_060312.1
14785	0.000492	cDNA FLJ37586 fis, clone BRCOC2005903. /gb=AK094905 /gi=21754065 /ug=Hs.141269 /len=2373	AK094905	Hs.141269	
14834	0.000743	component of oligomeric golgi complex 1 (COG1), mRNA /cds=(27,2969) /gb=NM_018714 /gi=21237782 /ug=Hs.283109 /len=3047	NM_018714	Hs.283109	NP_061184
14849	0.000135	cDNA FLJ11469 fis, clone HEMBA1001658. /gb=AK021531 /gi=10432731 /ug=Hs.224398 /len=1665	AK021531	Hs.224398	
14939	0.000492	control			